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## RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number:	09/937.009
Source:	PUT/09
Date Processed by STIC:	5/15/2002

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216. PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax) PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

http://www.uspto.gov/web/offices/pac/checker

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom. Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

- 1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>, EFS Submission User Manual ePAVE)
- 2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
- 3. Hand Carry directly to:

U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202

U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

 Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1803-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 01/29/2002

·	1477
ERROR DETECTED	SUGGESTED CORRECTION SERIAL NUMBER: 08/93/2006
ATTN: NEW RULES CASES	PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARF
1Wrapped Nucleics Wrapped Aminos	The number text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
2Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.
3Misaligned Amino Numbering	The numbering under each $S^n$ amino acid is cutally field. Do not use tab codes between numbers, use space characters, instead.
4Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
5Variable Length	Sequence(s) contain n's or Naa's representing more than one residue. Per Sequence Rules, each n or Naa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the < 220>-<223> section that some may be missing.
6Patentin 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please minually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
7Skipped Sequences (OLD RULES)	Sequence's)missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO.N: (insert SEQ ID NO where "X" is shown) (i)SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION SEQ ID NO N: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped
	Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to Include the skipped sequences.
8 Skipped Sequences (NEW RULES)	Sequence (s) missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000
9Use of n's or Xaa's (NEW RULES)	Use of n's and/or Naa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
10Invalid <213> Response	Per 1.823 of Sequence Rolles, the only valid <2135 responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <2205-<2235 section is required when <2135 response is Unknown or is Artificial Sequence
Use of <220>	Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.  Use of <220> to <223> is MANDATORY if <211> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic mut rial in <220> to <223> section.  ISee "Federal Register," 06.01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
r2Patentin 2 0 "bug"	Please do not use "Copy to Disk" function of Pate din version 2.0. This causes a corrupted file, resulting in missing manufactory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
Misuse of n	n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide
	AMCAMI. Protechedom Systems Branch - 08/21/2001

AMC/MH - Biotechnology Systems Branch - 08/21/2001



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        - 110> APPLICANT: Alessi, Dario
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                        Palendran, Anudharan
                          Leak, Maria
                           chirle, higahrd
                          Downes, Peter
                        Casamayor, Antonio
 10 <120 > TITLE OF INVENTION: Engyme
 13 1302 FILE PEFERENCE: 002.00170
 15 <140. CURRENT APPLICATION NUMBER: 09/937,009
 17 <141 CURRENT FILING DATE: 2000-03-13
 20 (150, PRIOR APPLICATION NUMBER: PCT/GB00/01004
 22 3151 PRIOR FILING DATE 2000-03-1
 25 <160: NUMBER OF SEO ID NOS: 21
35 -210: SEQ ID NO: 1
35 -211: LENGTH: 24
37 :212: TYPE: PST
39 :213: ORGANISM: Artificial Sequence
43 :220: FEATURE:
45 :223: OTHER INFORMATION: Description of Artificial Sequence (peptide)
49 :400: SEQUENCE: 1
51 Artificial Pro the Communication
 51 Arg Clu Pro Ard Ile Leu Ser Glu Gli Glu Glo Glo Met Phe Arg Asp
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 57
        Phe Asp Tyr fle Ala Asp Trp Cys
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 55 mil0: SEQ ID NO: 2
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131 - 211 LENGTH: 53
133 . 12
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135 - 213 - ORGANISM ( Artificial Sequence >
139 - 220. FEATURE:
141 - 223. OTHER INFORMATION: Pescription of Artificial Sequence(peptide
1:5 <400 > SEQUENCE: 4
        Mittasp Vin Tys Lys Wils Pr. Due Phe And Dec. - Add Trp Ser Act
153 Leu Met Asp Lys Lys Val Lys Pro Pro Phe Ile Pro Thr Ile Arg Gly
159 Arg Clu Asp Val Ser Ash Phe Asp Asp Glu Pho Thr Ser Glu Ala Pro
16: 35
165 lle Leu Thr Pro Pro
         5 C
173 -210: SEQ ID NO: 5
[75 - 311 LENGTH: 23
177 -: 212: TYPE PRT
179 -213 ORGANISM: Artificial Sequence
183 -220 FEATURE:
185 <223: OTHER INFORMATION: Description of Artificial Sequence peptide
189 <400. SEQUENCE: 5
191 Asp Glu Asp Ala Ile Lys Arg Ile Asp Gln Ser Glu Phe Glu Gly Phe
193 1
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197 Glu Tyr Ile Asn Pro Leu Leu
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205 HEIO, SEQ ID NO: 6
20" <211. LENGTH: 6
209 C212 - TYPE PRI.
211 <213: ORGANISM: Artificial Sequence
J15 - J10> FEATURE:
bit :223> OTHER INFORMATION: Description of Artificial Sequence peptide
211 9400 > SEQUENCE: 6
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203 s210 - SBQ 10 Not 8
265 W211 - LENGTHE 11
36" 212 - 1YPE: PET
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27% <220 FEATURE
274 x 227 OTHER INFORMATION: Description of Artifical Sequences people to
279 <400 SEQUENCE: 8
281 Pro his Phe Pro Glr. Phe Ser Thr Ser Ala Ser
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289 -210" SEQ ID Not 9
191 II. LENGTH: *
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295 1213: ORGANISM. Artificial Sequence
199 (220) FEATURE
701 - 223 OTHER INFORMATION: Description of Artificial Sequence peptite
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307 Thr Phe Cys Giy Thr Pro Glu Phe Leu
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315 (210) SEQ ID NO: 10
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319 42125 TYPE PRI
         2135 ORGANISM: Aftificial Sequence
321
 325 220 FEATURE
327 <223 OTHER INFORMATION: Description of Artificial Sequence peptide
331 <400 SEQUENCE: 10
333 Phe Glu Gly Phe Glu Tyr
335 1
341 <2100 SEQ ID NO: 11
243 (212) LENGTH: 13
145 (21.) TYPE PRI
347 21 ORGANISM: Artificial Sequence.
251 220 FEATURE:
353 (223) OTHER INFORMATION: Description of Artificial Sequence: peptide
357 (400) SEQUENCE: 11
359 Arg Gln Arg Tyr Gln Ser His Pro Asp Ala Ala Val Gln
375 1 1
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415 <2105 SEC ID NO: 14
417 *211 - LENGTH: 77
119 - 112: TYPE: PRT
421 <213> ORGANISM; Artificial Sequence
425 - 2201 FEATURE:
127 - 23 - OTHER INFOFMATION: Description of Artificial Sequences populate
141 - 400 - 3FG EN E: 14
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435 1
135 Lett Net Asp Lys Lys Val Lys Pro Pro Phe Ile Pro thr Ile Ary Gly
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451 The Leu Thr Pro Pro Arg Bla Pro Arg Ile Leu Ser Glu Glu Blu Gla
         50
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45" Glu Met The Ary Asp The Asp Tyr Ile Ali Asp Irp Tys
459 65
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465 | .210 - SEQ ID NO: 15
        Will: LENGTH: 77
467
469 -: 212: TYPE: PRT,
471 - 213: ORGANISM Artificial Sequence
475 -: 220: FEATURE:
477 (223) OTHER INFORMATION: Description of Artificial Sequence (peptide
181 |400: SEQUENCE: 15
483 Giu Asp Val Lys Lys Glm Pro Phe Phe And Thr Leu Gly Irp 31m Ala
489 Lou Leu Ala Ard Ard Leu Pro Pro Pro Fne Val Pro Thr Leu Ser Bly
491 20
495 Arg Thr Asp Val Ser Asm Phe Asp Glu Glu Phe Thr Gly Glu Ala Pro
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35
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557 Glu Ard Ard Pro His Phe Pro Oln Phe Ser Tyr Ser Ala Ser Thr Ala
554 65
511 -210: SEQ ID NO: 17
573 5211: LENGTH: 75
175 -212: TYPE: PRT
577 - 213: ORGANISM: Artificial Sequence
181 220 FEATURE
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587 <400: SEQUENCE: 17
389 Gly Clu Val Gin Ala His Pro Phe Phe Arg His Tle Asn Trp Glu Glu
5 6 1
The Leu Leu Ala Arg Lys Val Glu Pro Pro Phe Lys Bro Leu Leu Hin Ser
597
               .20
€01 Glu Glu Asp Val Ser Gln Phe Asp Ser Lvs Phe Thr Arg Gln Thr Pro
    3.5
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  " Mai Asp Ber Pro Asp Asp Ser Thr Low Ser Glu Ser Ala Ash Gin Val
    5.0
                           55
609
rl3 Phe Leu Gly Phe Thr Tyr Val Ala Pro Ser Val
                        70
   65
621 0210: SEQ ID NO: 18
623 (211): LENGTH: 82
h25 <212> TYPE: PRT
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631 (220" FEATURE
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639 Met Glu 11e Lys Ser His Val Phe Phe Ser Leu Ile Asn Irp Asp Asp
541 1
                                      10
645 Leu Ile Asn Lys Lys Ile Thr Pro Pro Phe Asn Pro Asn Val Ser Gly
ńΨ"
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651 Pro Asn Clu Leu Arg His Phe Asp Pro Glu Phe Thr Glu Glu Pro Val
65: 35
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##1 Dil-Cyfe: #Ff

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VERIFICATION SUMMARY

LATER APPLICATION US/09/937,009

COMPANDED TO THE TOTAL

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